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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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1836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_101002:*
1: /SIDS2/gcgdata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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1227.308 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	9	8	7	6	5	4	ω	N	1	No.	Result
1668.5	1668.5	1668.5	1691	1693	1699	1743	1777	1777	1836	Score	
90.9	90.9	90.9	92.1	92.2	92.5	94.9	96.8	96.8	100.0	Match Length DB	Query
455	455	455	352	383	341	341	394	394	350	ength	
18	18	17	22	22	22	22	23	22	22		
AAW29413	AAW29447	AAR95939	AAE08011	AAE08009	AAE08014	AAE08008	ABB79512	AAE08005	AAE08003	ID	
Human hippocampal	Human hippocampal	Human Y5 receptor.	Rat chimeric rNPY5	Dog chimeric cNPY5	Pig chimeric pNPY5	Dog chimeric cNPY5	Chimeric neuropept	Human chimeric NPY	Human chimeric NPY	Description	

Mouse chimeric mNP	AAE0801	22	508	79.6	1461.5	•
ശ		2 18			1511.5	
Rat neuropeptide Y	AAY14	20	445		1 15	
		18	445	82.7	1519	•
Rat neuropeptide Y	AAW15	18	445		1524	_
		21	445	83.1	1526	_
neuropeptide		20	445	83.1	1526	
neuropeptide		18	445	83.1	1526	_
Rat hypothalamic Y		20	456	83.7	1536	-
~		19	456	83.7	1536	-
Rat hypothalamic n		18	456	83.7	1536	
μY	AAW2944	18	456	83.7	1536	
Rat Y5 receptor.	AAR959	17	456	83.7	1536	
Chimeric rat/human	AAY52577	21	445	84.4	1549.5	
		22	445	•	1604.5	
Human chimeric NPY		22	499	87.7	1609.5	
S	AAE0285	22	445	87.7	1610.5	
		22	445	•	13	
	AAB85110	22	445		613	
		22	445	•	613	
		22	445	٠	w	
neur	AAE0792	22	445		ω.	
		21	445		w	
		20	445		ω ·	
		18	445		ω.	
neuropeptid		18	445		13.	
is domesti	AAW3709	19	456	88.0	1616.5	
chimeric	AAE0801	22	395		1637	
	AAE0801	22	383	•	S	
D)	AAE0801	22	455	٠	65.	
	ABB7951	23	455	٠	668.	
	AAE0800	22	455	٠	68.	
n hippoca	AAY 574	20	455	90.9	99	
Homo sapiens hippo	AAW37093	19	455		68.	

ALIGNMENTS

AAE08003 ID AAE(RESULT 1 Neuropeptide Y; NPY receptor: G-protein coupled transmembrane protein; transmembrane; TM domain; therapy; obesity; blood pressure; eiplepsy; Huntington's disorder; Parkinson's disorder; eating disorder; seizure; locomotor; anxiety disorder; limbic seizure; tranquilliser; N-PSDB; AAD14735 WPI; 2001-514543/56 02-AUG-2001. WO200155103-A2 Human chimeric NPY5deltaY1IC3 receptor. 01-NOV-2001 (first entry) Bennett M, (NEUR-) 28-JAN-2000; 2000US-0178652 29-JAN-2001; 2001WO-US02804. Homo sapiens. human; chimeric receptor. AAE08003 standard; Protein; NEUROGEN CORP Brodbeck ₽, Krause J; 350 AA

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RESULT 2
AAD600505
ID AAD600
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XX AAC
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                                      02-AUG-2001
                                                                                                            WO200155103-A2
                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                       transmembrane; TM domain; therapy; obesity; blood pressure; eiplepsy; Huntington's disorder; Parkinson's disorder; eating disorder; seizure locomotor; anxiety disorder; limbic seizure; tranquilliser;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to chimeric neuropeptide Y (NPY) receptor. The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE08005 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is human chimeric NPY5deltaYIC3/deltaYIC7 receptor. The chimera comprises intracellular loop 3 and C-terminal intracellular domain of NPY5 receptor respectively, of NPY1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to chimeric neuropeptide Y (NPY) receptors The NPY receptors are 6-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric receptor proteins amino acids, useful as targets discovery and development -
                                                                                            ABB79512
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)B; AAD14737.
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                                                                                             standard;
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                                                                                             Protein;
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99.4%;
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Pred. No. 1.4e-181;
L; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a single polypeptide chain for drug actions, and as basis for dru
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain of NPY5 receptor
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Chimeric neuropeptide receptor hNPY5deltaY1IC3/deltaY1CT

23-SEP-2002 ABB79512

(first entry)

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Query Match
Best Local S
Matches 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bakthavatchalam R, Bl
Hutchison A, Tran J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders, e.g. eating disorders such as obesity or psychiatric disorders, diabetes and cardiovascular of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-spiroisobenzofuran-1,4'-piperidine, useful for treating, e.g. disorder, psychiatric, cardiovascular disorder or diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuropeptide Y5; NPY; NPY5; NPY1; receptor; antagonist; antiinflammatory; nootropic; neuroprotective; cardiovasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEUROGEN CORP.
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                                                   HTSVCIRLKRRNNMMDKMRDNKYRSSRSVFYRLTILILVFAVSWMPLHLFHVVTDFND
                                                                                                                                      CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
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HTSVCIRLKRRNNMMDKMRDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFND
                                                                                                            CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
                                                                                                                                                                                                                       KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180
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99.4%;
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X, Elliott RL,
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1.4e-181;
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                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to chimeric neuropeptide Y (NPY) receptors The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that
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                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennett M,
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                                                                                           11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
                                                                                                                                      Local Similarity
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LILMALMKKRNOKTTVNFLIGNLAFSDILVVLECSPETLTSVLLDQWMEGKVMCHIMPFL 130
                                                             MDLELQDFYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                               Page 58-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brodbeck R,
                                                                                                                                                                                   341 AA;
                                                                                                                      Conservative
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                                                                                                                                      94.98;
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                                                                                                                           Score 1743; Db 22,
No. 5.2e-178;
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Matches 320
                                                                                                                                                              The NPY receptors are G-protein coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is pig chimeric pNPY5deltapY1IC3 receptor. The chimera comprises intracellular loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
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    The present invention relates to chimeric neuropeptide Y (NPY) receptor The NPY receptors are 6-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane; TM domain; therapy; obesity; blood pressure; ei
Huntington's disorder; Parkinson's disorder; eating disorder;
locomotor; anxiety disorder; limbic seizure; tranquilliser;
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          discovery
                    New chimeric receptor proteins comprising a single polypeptide chain amino acids, useful as targets for drug actions, and as basis for drug actions.
                                                                                                                                                                                                                                                                     Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane transmembrane; TM domain; therapy; obesity; blood pressure; eithuntington's disorder; Parkinson's disorder; eating disorder; locomotor; anxiety disorder; limbic seizure; tranquilliser; rat; chimeric receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VELQETFDSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKR
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          and development
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Pred. No. 1.4e
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1.4e-172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drug actions, and as basis for drug discovery and development. The NPY5 receptor may have an anti-epileptic activity in the control of limbic seizures. The present sequence is rat chimeric rNPy5deltarYIIC3 receptor. The chimera comprises intracellular loop 3 of NPY5 receptor replaced with intracellular loop 3 of NPY1
                                                                                                                                                                             Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior; G protein-coupled receptor; agonist; antagonist; obesity; bulimia; anorexia; transgenic animal.
                                                                                                                           Key
                              Domain
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                                                                                                                                                                                                                                                                                            AAR95939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHSLVELKETFGSALLSSKYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCI
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                                                                                                             Location/Qualifiers 51..77
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92.4%;
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Matches 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human hippocampal Y5 receptor (AAR95939) was identified as the homologue of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1 receptor'. The receptor belongs to the G protein-coupled receptor superfamily. It is encoded by a cDNA clone (see also AAT30433) that was isolated from a hippocampus cDN library using rat Y5 receptor cDNA as probe. Recombinant rat Y5 receptor can be produced in prokaryotic or eukaryotic (e.g. COS, 293 or Sf9 insect) host cells. It is used to identify Y5 ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying increases
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hes 333;
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                                                                                                                                                                                                                     CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                using Y5 receptor (ant)agonists - consumption, for treatment of e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1668.5; DB 17; Length Pred. No. 7.3e-170;
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Query Match
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90.9%;

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7.3e-170; hes 11; I

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                         a warm-blooded animal, including man, in need of such treatment a therapeutically effective amount of a quinazolin-2,4-diazirine compound. These disorders and diseases include e.g. eating disorders, obesity, bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, pain, sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage, shock, congestive heart failure, nasal congestion or diarrhoea.
                                                                                                                                   The present sequence represents human hippocampal neuropeptide (NP) Y receptor subtype Y5, with a pharmacological function associated with for example, obesity and eating disorders. The specification relates to a method of treatment and prophylaxis of disorders and diseases to a method with with NPY receptor subtype Y5 comprising administering to associated with with NPY receptor subtype Y5 comprising administering to
Sequence
                                                                                                                                                                                                                                                                Use of new and known quinazolin-2,4-diazirine compounds as NPY receptor antagonists - for treating and preventing eating disordiabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures, migraine, sleep disturbance, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hippocampal; neuropileptic seizuro
eating disorder;
                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-319712/29
                                                                                                                                                                                                                                                                                                                                                                                          Tintelnot-blomley M;
                                                                                                                                                                                                                                                                                                                                                                                                          Schmidlin
                                                                                                                                                                                                                                                                                                                                                                                                                       Criscione
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                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT89114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human hippocampal neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW29447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seizure; migraine; sleep disturbance;
sorder; quinazolin-2,4-diazirine.
                                                                                                                                                                                                                                   Pages 127-129; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropeptide Y Y5 receptor; NPY Y5;
                                                                                                                                                                                                                                                                                                                                                                                                          Tintelnot-blomley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                          ס
                                                                                                                                                                                                                                                                                                                                                                                                        Rueger H, Schilling ley M, Yamaguchi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y Y5 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis;
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                                                                                                                                   Criscione L,
                    Disclosure;
                                                     diabetes,
                                                                                                                                                                                                                                                                                                         bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory lo epileptic siezure; migraine; sleep disturbance; pain; depression; sexual disorder; anxlety; cerebral haemorrhage, shock; diarrhoea; congestive heart failure; eating disorder; obesity.
                                                                Use of new and known hetero:aryl compounds as NPY Y5-receptor antagonists - for treating and preventing eating disorders,
                                                                                                 N-PSDB; AAT89110.
                                                                                                                                                                                             01-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                             Human hippocampal neuropeptide Y Y5 receptor
                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW29413 standard;
                                                                                                                                                                     (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                  18-NOV-1996;
                                                                                                                                                                                                                                          12-JUN-1997
                                                                                                                                                                                                                                                               WO9720820-A1
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180
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                                          dyslipidaemia,
etc.
                     Pages 76-78;
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                   Tintelnot-blomley
                                                                                                                                               Rigollier P,
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                                                                                                                                                                                            95US-0566349
                                                                                                                                                                                                                   96WO-EP05055
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 455
                   155pp;
                                                     hypertension,
                                                                                                                                  Rueger
lley M,
                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                    H, Schilling
Yamaguchi Y;
                                                                                                                                   Yamaguchi
                                                     memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455
                                                     loss, epilepsy
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This sequence

represents

human hippocampal neuropeptide

(NP)

Y receptor

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AAW37093
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AC AAW3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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Matches
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     21-FEB-1997;
                                                        04-JUN-1997;
                                                                                                                                                                                                                                                                               Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity; feeding behaviour; modification; atypical neuropeptide.
                                                                                                                                                                     W09746250-A1
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens hippocampal Y5
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                                                                                                                11-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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73.2%;
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Pred. No. 7.3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be used to treat obesity and activators can be used to treat anorexia. Antagonists capable of alleviating (by decreasing the activity of Y5-R) an abnormality can be identified by administering a potential antagonist to a transgenic mammal as above, and determining whether the substance alleviates the physical and behavioural abnormalities displayed by the transgenic mammal as a result of overactivity of a Y5-R. Agonists can be identified in a similar manner, but where the abnormality is alleviated by increasing the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y5-r can be used in processes to determine whether a chemical compound specifically binds to and activates or inhibits a Y5-R by measuring a second messenger response. The chemical compounds can be used to increase or reduce the activity of a Y5-R. In particular, inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding canine hypothalamic atypical neuro:peptide Y/peptide receptor, \gamma S - useful for identification of compounds which are capable of modifying feeding behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                             HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM
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Pred. No. 7.3
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The present sequence represents the human hippocampal Y5 receptor. The Y receptor is a G-protein coupled neuropeptide Y receptor found throughout the mammalian nervous system and is a powerful stimulant of feeding behaviour. Cells expressing DNA encoding the Y5 receptor can be used to determine whether a ligand specifically binds to a Y5 receptor. These cells or a cell extract, is exposed to the ligand and then any binding between the ligand and the receptor can be detected. The cells can also be used to determine whether a ligand is a Y5 receptor antagonist or agonist. The binding of chemical compounds to a Y5 receptor can also determined and whether they activate or inhibit the activation of the Y5 receptor can also be determined using cells expressing the receptor. The effect of drugs on the Y5 receptor and whether they act as agonists or a y5 receptor.
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                                                                                                                              KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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                                                                                                                                                                                                                                                                                                                                          VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFG
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Pred. No. 7.3e-170;
6; Mismatches 11;
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transmembrane; TM domain; therapy; obesity; blood pressure; eiplep
turansmembrane; TM domain; therapy; obesity; blood pressure; eiplep
thuntington; disorder; parkinson; disorder; eating disorder; ser-
locomotor; anxiety disorder; limbic seizure; tranquilliser; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuropeptide Y5 (NPY5)
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                                                                            NEUROGEN CORP
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                                      Brodbeck R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The NPY receptors are G-protein-coupled transmembrane proteins with seven membrane spanning transmembrane (TM) domains. The compounds that modulate the activity of a NPY receptor is useful in the preparation of a medicament for treating conditions including obesity, high/low blood pressure, epilepsy, Huntington's and Parkinson's disorder and eating, seizure, locomotor and anxiety disorders. They can also be used as targets for drive actions.
Neuropeptide Y5; NPY; NPY5; receptor; human; antagonist; anorectic; antiinflammatory; noutropic; neuroprotective; cardiovascular; hypotensive; antidabetic; psychiatric; anticonvulsant; cardiant; cerebroprotective; antidepressant; haemostatic; tranquillizer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders, e.g. eating disorders such as obesity or bulimia, psychiatric disorders, diabetes and cardiovascular disorders such as hypertension, in humans and animals.
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)B; ABN84252.
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SSRSRSVFYRLTILILVFAVSWMPLHLEHVVTDFNDNLISNRHFKLVYCIC
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J, Zheng
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Best Local
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                                                                                                                                               Sequence
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Huntington's disorder; Parkinson's disorder; eating disorder;
locomotor; anxiety disorder; limbic seizure; tranquilliser;
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O99k73 macaca mula
O925f1 cavia porce
O89fm2 gallus gallu
O99k75 macaca mula
O99k71 gallus gall
O99k71 gadus morhu
O57463 brachydanio
O8uvw7 lampetra fl
O9705 sus scrofa
O73734 brachydanio
O922d4 cavia porce
O9erc0 rattus norv
O967t7 drosophila
O8sz35 drosophila
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365 5 09XVIA 365 11 09DBV6 367 12 09NHA4 399 5 020067 423 5 0944D4 423 5 09T8D1 357 5 09NEC8 391 5 09CZG8 391 5 09UZG8 398 4 09UZG1 398 4 09UZG1 398 4 09UZG1 398 4 09UZG1
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NPY receptor 5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
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EMBL; AR535240.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
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Lundell I., Eriksson H., Marklund U.,
"Cloning and characterization of the
receptor Y5.";
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                                          QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
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                                                                                                                                                                                                                                               PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                          446 AA; 50936 MW;
                                                                                                                                                                                Conservative
                                                                                                                                                                                        86.6%;
71.5%;
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19,
20,
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Last sequence update)
Last annotation update)
                                                                                                                                                                              Score 1589.5; I
Pred. No. 8.6e-J
9; Mismatches
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                                                                                                                                                                                                                         2C3984B0A90AA693 CRC64;
                                                                                                                                                                                                                                                                                                              guinea pig neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 AA
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                                                                                                                                                                                        DB 11; Length 446; -127;
                                                                                                                                                                             13; Indels 105;
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	5 LNPILYGFLNNGIKADLVSLIHC 347	325	νQ
	RSRRVFCRLTVLILVFGFSWMPLHLFHIVTDFNATLISNRHFKLVY	357	Db
	SRSVEYRLTILILVFAVSWMPLHLFHVVTDENDNLISNRHFKLVYCICHLLGMMS	265	Qy
	7 LRQQQDADFRDLPETSGTEKSQLSSSSKFIPGVPICFEMKPEENTEIQDMITVSQSIIRI 356	297	дь
	7KMRDNKYR 264	257	Qy
	7 RLSSKEGKFQENEMINLTLHPSKSAGTEAQPSSHTSWSCALVRKHHRRYSKKTSTVMPAI 296	237	Db
		25	Qy
	7 VDLHKTLNLEALENRLLCIESWPSDSYRIAFTISLLLMQYILPLVCLTASHTSVCRSVGS 236	177	ДD
	VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIR	193	Qy
		117	Db
	1 OCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVF	13	у
	8 LVLTAL-TKRKQKTIINILIGNLAFSDILVVLFCSPFTLTSVLLDRWMFGTVMCHIMPFL 116	5	da
	_ 	7	Qy
	LGFK		Db
	1 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFV:	₩.	Qу
6	Match 66.4%; Score 1219; DB 13; Length 443; LOCAL Similarity 55.5%; Pred. No. 2.1e-95; LOCAL SIMILARITY SOLUTION SOL	Query M Best Lo Matches	
	EQUENCE 443 AA; 50044 MW; EFE9F1A391CC092E CRC64;	ω	SQ
	tor.	Re	KW
	arochem. 81:462-471(200	17 C4 1	D R
	<pre>nacological characterization of cloned chicke tors y1 and y5.";</pre>	H =	RT
	ence from N.A. Derg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D	æ v	RA
		3 = 2	RN
	-		2 6
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		88
	(Chicken).		88
	receptor Y5.		DE
	rEMBLrel. 21, Last sequence update)		DI
	rEMBLrel. 21. Cre		DI AC
	PRELIMINARY; PRT; 443 AA.	2	ID
•		ESULT 3	RE
	1 NPILYGFLNNGIKADLMSLIHC	42	Dξ
	6	32	Qy
	1 KRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCC	36	Дb
	7 -RS	26	Qy
)1 ARPSLENQSRTLPENFGSVRSQISSSSKFIPGVPTCFEIKPEDNSDAHEMRVKRSITRIK 360	30	Db
	57 266	26	Qy
	1 GLSNKENRLEENEMINLTLHPSKKSGNQVKLSKTHK	24	ДD
	16	24	Qy

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RESULT
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T 01-JUN-2002 (TrEMBLrel. 21, L. T 01-JUN-2002 (TrEMBLrel. 21, L. T 01-JUN-2002 (TrEMBLrel. 21, La Neuropeptide Y receptor Y1. Gallus gallus (Chicken) Eukaryota; Metarr
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Best Local S
Matches 130
                                                                                             Q8QFM1;
Q8QFM1;
Q1-JUN-2002
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Q1-JUN-2002
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MEDLINS-21184974; PubMed-11287088;
Gehlert D., George C., Wang Y., Schober D.,
Gackenheimer S., Johnson D., Beavers L.S., Gadski R.A.,
"Cloning and characterization of Rhesus monkey neuropept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Neuropeptide Y receptor Y1.
Neuropeptide Y receptor Y1.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subtypes(1).";
Peptides 22:343-350(2001).
EMBL; AF303089; AAG40771.1;
InterPro; IPR002276; GPCR_Rhodpsn.
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NCBI_TaxID=9544;
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                                                                                                                                                                                             PRELIMINARY;
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                             Craniata;
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                             Vertebrata;
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                           Euteleostomi;
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073733;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Neuropeptide Yypeptide YY receptor Ya.
                    SEQUENCE FROM N.A.

MEDLINE-98096393; PubMed-9434780;

Ringvall M., Berglund M.M., Larhammar D.;

"Multiplicity of neuropeptide Y receptors:

subtype in the zebrafish.";

Biochem. Biophys. Res. Commun. 241:749-755(
                                                                                                      Larhammar D.;
"Cloning and characterization of a subtype in the zebrafish.";
nNA Cell Biol. 16:1357-1363(1997).
                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmberg S.K.S., Mikko S., Boswell "Pharmacological characterization receptors Y1 and Y5.";
J. Neurochem. 81:462-471(2002).
EMBL; AY040845; AAK83557.1; ...
Receptor.
                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=98068842; PubMed=9407007;
                                                                                                                                                                                                                                                                                    NPYRYA OR NPYRYA
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[1]
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SEQUENCE
                                                                                                                                                                 Lundell I., Berglund
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIINPRGWRPNNRHAYMGIAAIWVLATASSLPFLIYHVLTD--EPFRNITFDEYKDKYVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRINIMLISIVVAFAVCWLPLTIFNIVFDWNHEILPVATCSHNLLFLICHLTAMISTCVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNSQILQFEDEDCHVPLAMVFTLALAYGTVIILGVSGNLALIVIILKQKEMRNVTNILIV
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FROM
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М
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                        Commun. 241:749-755(1997).
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                                                                                                                                                                 Starback P.,
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                                                                                                                                                                                                                                           h) (Zebra danio).
a; Craniata; Verte
; Teleostei; Osta
                                                                                                                                                                                                                                                                                                                                                                                                                             341
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                                                                                                                                          novel
                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
                                                                                                                                                                 Salaneck
                                                                                                                                        neuropeptide
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                                                cloning
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                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                              Cypriniformes;
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Best Local S
Matches 124
           Query Match
Best Local 9
 Matches
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                                                                  Lundell I., Boswell T., Larhammar D.; "Chicken Neuropeptide Y Family Receptor Y4; a Receptor with Equal Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide Y Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF410853; AAL84161.1; -.
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SEQUENCE
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Starback P., Lundell I., Fredriksson R., Berglund M.M., Wraith A., Soderberg C., Postlethwait J.H., Larhammar D. "Neuropeptide Y receptor subtype with unique properties zebrafish: the zYa receptor.";
Brain Res. Mol. Brain Res. 70:242-252(1999).
EMBL; AF037400; TAGO
                                                SEQUENCE
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                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                               NCBI_TaxID=9031;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSTLTHNQSNSSLFLLDVPCW---QSSTMTLT--LVLCYCLVLILGLIGNILLICIIMHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNLLILMALMKK
 119;
                                                                                                                                                                                                                                                                                                                                                                                                 SRNREDEHRRVMHSKRINVMLATLVAAFAVCWLPLNAFNVVADCDQEVLPVCNHNLLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                       ----RDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLVLIALERHQLILHPSGWKPSVPQAYIAVLTVWLLACVTSLPFLAFHLLTSEPYSLFP
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Pro; IPR000276; GPCR_Rhodpsn
PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124;
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              Similarity
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 Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Α.,
                                                                                                                                                                                      Neognathae;
                                                                                                                                                                                     Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42901 MW;
            31.5%;
                                                  42972 MW;
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 78;
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                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 617.5;
Pred. No. 1.7
            Pred. No. 3.9e-41;
                        Score 578;
                                                                                                                                                                                                                                                                                       PRT;
                                                C9EC6C00DBFD1F9E
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 Mismatches
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                        DB 13;
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 129;
                                                                                                                                                                                     Phasianidae;
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                                                CRC64;
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Indels
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                         377;
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                                                                                                                                                                                     Phasianinae;
18;
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Gaps
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Gadus morhua (Atlantic cod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebr
Actinopterygii; Neopterygii; Teleostei; Eutelec
Acanthomorpha; Paracanthopterygii; Gadiformes;
                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                            Arvidsson A.K., Wraith A., Jonsson-Rylander A.C., Lark "Cloning of a neuropeptide Y/peptide YY receptor from cod: the Yb receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YHX1;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last seque)
Q1-MAR-2002 (TrEMBLrel. 20, Last annot)
Neuropeptide Y/peptide YY receptor Yb.
                                                                                                                                                                                                                                                                                                                      Regul. Pept. 75:39-43(19
EMBL; AF073925; AAD02833
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=99017378; PubMed=9802392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9YHX1
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                 Receptor
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                                  IWVVACLISVPFLSFTVLDNLP----LQNLSLPFPG---QDHWLCTESWPTNSNRLAYTT
                                                                                   LMDRWILGEALCKLTPFVQCISVTVSIFSLVLIAMERYQLIIHPTGWKPMVGQSYMAVGI
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                                                                                                                                                                                                                                    374 AA;
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                                                 LGFAICSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTI
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67;
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                                                                                                                                                                                               Score 554.5; DB 1
Pred. No. 3.7e-39;
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Euteleostei; Neoteleostei;
=
                                                                                                                                                                                                                                                             UNKNOWN_1.
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RESULT 10
Q8UVW7
ID Q8UVW
AC Q8UVW
DT 01-MA
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057463
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Best Local S
Matches 101
  Q8UVW7
Q8UVW7;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subtype in the zebrafish.";

DNA Cell Biol. 0:0-0(1997).

EMBL; AF030245; AAB94616.1; -

ZFIN; ZDB-GENE-980526-208; npyryb.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
Neuropeptide Y /peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O57463;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   057463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lundell I., Be
Larhammar D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                    MPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADLVSLI 345
                                                                                                                                                                                                                                                                    VQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSR-SRSVFYRLTILILVFAVSW 286
                                                                                                                                                                                                                                                                                                                                                    VWTLGFAICSPLPVFHSLV-----ELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KATLSHC 338
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                                                                                                                                                              LPLNVFNTIFDWNHEAIPVCQHDAIFSACHLTAMASTCVNPVIYGFLNNNFQKELKSLL
                                                                                                                                                                                                                                             COYCLPLALILVCYFRIFLRLSRRKDMVERARGGROKKAKGSKRVNAMLASIVAAFALCW
                                                                                                                                                                                                                                                                                                                           IWITACFISLPFLSFNILTNSPFHNLSLPFNP--FSDHFICIEQWPSEGNRLTYTTTLLL
                                                                                                                                                                                                                                                                                                                                                                                                         LMDRWILGEALCKVTPFVQCMSVTVSIFSMVLIALERHQLIIHPTGWKPVVRHSYLAVAV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                               LLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLIVAYSTMLAVGLVGNTCLVVVITRQKEMRNVTNIFIVNLSCSDILVCLVCLPVTIIYT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVCWLPLNIFNTVFDWHHELMVSCQHNLIFSVCHLVAMASTCVNPVVYGFLNSNFQKQL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLVFQYFLPLGLIAACYLSIFLRLRRRKDMVERARDSSRDNRAKGSRRINVMLGSIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.4%; Score 539; DE 33.8%; Pred. No. 7.7e tive 68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06, Created)
06, Last sequence update)
19, Last annotation update)
YY receptor Yb.
  20,
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Created)
Last sequ
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                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4B0C9551131A14D1 CRC64;
  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel neuropeptide
                                                             365
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7.7e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 375;
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RESULT 11
097505
ID 09750
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COLUMN NEW Y Y
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                   097505
097505;
                                                  STRAIN=LWD; TISSUE=KIDNEY;
Ito Y., Minezawa M.;
"Sus scrofa NPY Y4 gene for neuropeptide Y receptor type
                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Neuropeptide Y receptor type 4 (Neuropeptide Y-family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam: pF00001; 7tm_1; 1.
prints; pR00237; GPCRRHODOPSN.
pROSITE; pS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
prOSITE; pS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21590343; PubMed=11733009; Salaneck E., Fredriksson R., Larson E.T., Conlon J.M., Larhammar D. "A neuropeptide Y receptor Y1-subfamily gene from an agnathan, the European river lamprey. A potential ancestral gene."; Eur. J. Blochem. 268:6146-6154 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 268:6146-6:
EMBL; AF340022; AAL66410.1;
                   Submitted (DEC-1998) to the
                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                             NPY Y4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. NPY receptor.
                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lampetra fluviatilis (River lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308
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                                        [genomic]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRD---NKYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVE-----LQETFGSALLSSRYLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDFPVWD-DYKSSVDDLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPIFYGFLNNNFLKELKATILRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPTGWKPSLNHAYVAIGAIWVAAFAMSSPFLAFHVLTDEPYRNLSHYFPD--YGEKVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFSDMLVGLVCLPLTIAYTLMDHWIFGEALCKGSPFLQCSAVSVSIFSLVLIAIERHQLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I EVVALGHLKFAFTTSLLVFQFSCPLLFVFLCYLRIFLRLRQRKKMLPTGREGGGNGVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41060 MW;
                                                                                                                                                                             Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.9%;
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                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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1.6e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 365;
                                                                                                                                                                                 Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                     receptor
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Gaps

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187 208

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EMBL; AF227955; AAF62507.1; -.
InterPro. IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UN
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
Neuropeptide; Receptor.
                                                                                                                                                                                                 O73734 PRELIMINARY; PRT; 373 AA.
O73734;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence up
O1-DEC-2001 (TrEMBLrel. 19, Last annotation
Neuropeptide Y/peptide YY receptor YC.
NPYRYC OR NPYRYC.
     SEQUENCE FROM N.A. MEDLINE=98096393; PubMed=9434780;
                             "Cloning and characterization of a
subtype in the zebrafish.";
DNA Cell Biol. 16:1357-1363(1997).
                                                                                                   SEQUENCE FROM N.A. MEDLINE=98068842; PubMed=9407007;
                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                       Lundell I.,
                                                                                                                                          NCBI_TaxID=7955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary Andersson L., Lundin L.-G., Larhammar D.; "Evolution of the neuropeptide Y receptor family: gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BREED NORWEGIAN LANDRACE;
MEDLINE-20187975; PubMed-10720571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide;
SEQUENCE 37
                                                                              Jarhammar D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPL-----PVFHSLVELQETFGSA
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                                                                                      Berglund
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Μ.
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RESULT 13

Q9Z2D4

Q9Z2D

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Best Local S
Matches 100
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hes 100;
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Sharma P.S., Holmberg S.K., Briksson H., Beck-
Grundemar L., Larhammar D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL: AF072822; AAD13144.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN
PROSITE; PS00237; G_PROTEIN_R
                                                                                                                                                                                                                                           "The cloned guinea pig pancreatic more the human Y4 than does the rankegul. Pept. 75:29-37(1998).
                                                                                                                                                                                                                                                                                                                              MEDLINE=99017377; PubMed=9802391; MEDLINE=99017377 H. Berglund M.M., Holmb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sec
01-MAR-2002 (TrEMBLrel 20), Last an
Pancreatic polypeptide receptor Y4
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Crani
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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"Multiplicity of neuropeptide Y receptors: cloning of a third distinct subtype in the zebrafish.";
Biochem. Biophys. Res. Commun. 241:749-755(1997).
EMBL, AF037401; AAC41277.1; -.
ZFIN: ZDB-GENE-990415-775; npyryc.
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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G_PROTEIN_RECEP_F1_1;
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33.2%; Pred. No. 7.5%
Live 72; Mismatches
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(CSTRAIN-WISTAR; TISSUE-SMALL INTESTINE;

(A VOISIN T., Goumain M., LaBurthe M.;

(Toning of a CDNA encoding a rat type 2 neuropeptide Y/peptide YY

(Teceptor expressed in intestinal epithelial crypt cells.";

(L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.)

(EMBL; AY004257; AAF89094.1; -

(EMBL; AY004257; AAF89094.1; -

(EMBL; AY004257; FRO10120; Lectin_legB.

(FINTESPRO) IPR010276; GPCR_Rhodpsn.

InterPro; IPR010120; Lectin_legB.

(FAINTS; PR000217; Thm_l; 1.

(FAINTS; PR00237; GPCRRHODOPSN.

(FAINTS; PR01570; MOFFPRECEPPOR.

(FAINTS; PR01570; MOFFPRECEPPOR.

(FAINTS; PR01570; GPCRTEIN_RECEP_F1_2; UNKNOWN_1.

(FAINTS; PS01237; G_PROTEIN_RECEP_F1_2; 1.

(FAINTS; PROTEIN_RECEP_F1_2; 1.

(FAINTS; PS01237; G_PROTEIN_RECEP_F1_2; 1.

(FAINTS; PROTEIN_RECEP_F1_2; 1.

(FAIN
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 98; Conserv
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Best Local
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neuropeptide Y/peptide YY-Y2 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ERC0;
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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   109
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   LTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF
                                                                                                           DLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSKALAFLEDKVACKESWPLGHHRVVYTTFLLLFQYCIPLAFILVCYLRISWRLRROGRV
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                                                                   EVQVVLILAYCSIILLGVVGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KANVTSLLIANLAFSDFLMCLICQPLTVIYTIMDYWIFGEVLCKMSAFIQCMSVTVSILS 131
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                                                                                                                                                                                                                                                                                                                                            381
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                            42510 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia;
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31.1%;
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Pred. No. 1
                                                                                                                                                                                                Score 503; DB 11;
Pred. No. 8.8e-35;
5; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                            659327904B288BC7 CRC64;
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L.5e-35;
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Best Local S
Matches 107
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"Characterization of a functional neuropeptide F receptor
T Drosophila melanogaster.";
L Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF364400; AAK50050.1; -.
R FIYBase; FB9n0037408; NPFR1.
R InterPro; IPR000276; GPCR_Rhodpsn.
R Pfam; PF00001; 7tm_1; 1.
R Pfam; PF00001; 7tm_1; 1.
R Pfam; PF00001; 7tm_1; 1.
R PRINT'S; PR01570; NPEFRECEPTOR.
R PRINT'S; PR01570; NPEFRECEPTOR.
R PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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Q967T7;
Q1-DEC-2001
Q1-DEC-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Garczynski S.F. Jr., "Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide F
NPFR1 OR CG1147
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                                                                                                                                                                                                                                                               133 VSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVE
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                                               RLKRRNNMMDKMRDNKYRS-SRSRSVFYRLTILI---LVFAVSWMPLHLFHVVTDFNDNL
                                                                                                     --NTDTPALLQQIGLQDTIPYCIEDWPSRNGRFYYSIFSLCVQYLVPILIVSVAYFGIYN
                                                                                                                                                    LQETFGSALLSSRYL-----CVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCI
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31.2%; Pred. No. 1.
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Last annotation update)
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Run on:
                                                                                                   OM protein - protein search, using sw model
                                                      November 22,
                                                                                                                                                                        GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
2002, 13:05:43; Search time 14 Seconds (without alignments)
1036.908 Million cell updates/sec
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Title: Perfect score:

Sequence: US-09-771-956-6 1836 1 MSFYSKQDYNMDLELDEYYN.....GFLNNGIKADLVSLIHCLHM 350

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched:

Total number of hits satisfying chosen parameters: 112892

112892 seqs, 41476328 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34
337	337	339	341	341	344.5	354	358.5	361.5	365.5	366	372.5
18.4	18.4	18.5	18.6	18.6	18.8	19.3	19.5	19.7	19.9	19.9	20.3
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ALIGNMENTS

	RP RA	RESULT NYSR_H ID NY AC Q DT 0 DT 10 DE N DE N DE N OC N OC M
Flores-Riveros J. R., Friedman L. Jiang P., Lewis-Higgins L., Sadlowski Y., Schaefer J., Velazquez N., McCaleb M.L.; "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior."; J. Biol. Chem. 271:26315-26319(1996). 3] SEQUENCE OF 11-455 FROM N.A. MEDLINE-97312686; pubMed-9169127; Herzog H., Darby K., Ball H., Hort Y., Beck-Sickinger A., Shine J.; "Overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation."; Genomics 41:315-319(1997)	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUB-Hippocampus; MEDLINE-96317589; PubMed-8700207; Gerald C., Walker M.W., Criscione L., Gustafson E.L., Gerald C., Walker M.W., Criscione L., Gustafson E.L., Batzl-Hartmann C., Smith K.E., Vaysse P., Durkin M.M., Laz T.M., Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G., Taber R.I., Branchek T.A., Weinshank R.L.; "A receptor subtype involved in neuropeptide-Y-induced food intake."; "A receptor subtype involved in neuropeptide-Y-induced food intake."; Nature 382:168-171(1996). [2] SEQUENCE OF 11-455 FROM N.A. MEDLINE-96421636; PubMed-8824284;	LIT 1 LHUMAN NY5R_HUMAN STANDARD; PRT; 455 AA. Q15761; Q92916; Q1-NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5) Preceptor) (NPYY5) Proceptor) (NPYY5) NPY5R OR NPYR5. HOMO Saptens (Human). BUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NOBI_TaxID=9606;

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                                                                                                                      KKTACVLPAPERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHEL
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                                                HLLGMMSCCLNPILYGFLNNGIKADLVSLIHCLHM
                                                                                    RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC
                                                                                                                                                           HTSVCRSISCGLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYS
                                                                                                                                                                              HTSVC----IRLKRRNNMMDK------
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333; Conser
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00001; 7tm_1; 1.

00001; 7tm_1; 1.

ESO0237; G_PROTEIN_RECEP_F1_1; FALSE_NEG
PS50262; G_PROTEIN_RECEP_F1_2; 1.

n. coupled receptor; Transmembrane; Glycop.
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AAC50741.1;
AAC51295.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor) (NPYY5).
NPY5R OR NPY5.
Canis familiaris (Dog).
Cunis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Camamalia; Eutheria; Carnivora;
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Regul. Pept. 75:4
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-protein
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Borowsky B., Walker M.W., Bard J., Weinshank R.L
Vaysse P., Branchek T.A., Gerald C.;
"Molecular biology and pharmacology of multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-99017379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIGHEST TO TACHYKININS RECEPTORS.
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00237;
PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG
PS50262; G_PROTEIN_RECEP_F1_2; 1.
    coupled receptor; Transmembrane; Glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                      446
    Conservative
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                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein;
                      86.1%;
71.7%;
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                                                                                                                                                                                                                                                         5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                        CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
BY SIMILARITY.

PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               3 (POTENTIAL).
CYTOPLASMIC (F
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (PC
2 (POTENTIAL).
EXTRACELLULAR (
Score 1581.5; DB 1
Pred. No. 1.3e-90;
7; Mismatches 14;
                                                                                                                                                                                                                   EXTRACELLULAR 7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmitate.
                                                                                    SCAC8D2FCF5D254A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weinshank R.L.,
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                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                         (POTENTIAL)
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EMBL outstation -
trictions on its
    105;
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  Gaps
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Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins Sadlowski Y., Schaefer J., Velazquez N., McCaleb M.L.; "Identification of a novel hypothalamic neuropeptide Y recrassociated with feeding behavior."; J. Biol. Chem. 271.26315-26319(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       063634: P70586;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
Neuropeptide Y receptor type 5 (NPY5-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerald C., Walker M.W., Criscione L., Gustafson E.L., Batzl-Hartmann C., Smith K.E., Vaysse P., Durkin M.M., Laz T., Linemeyer D.L., Schaffhauser A.O., Whitbread S., Hofbauer K. Taber R.I., Branchek T.A., Weinshank R.L.;

"A receptor subtype involved in neuropeptide-y-induced food in Nature 382:168-171(1996).
                                                                                                                                                                                                                                                                       neuropeptide Y are potent neuropeptide Y neuropeptide Y Y4 receptor agonists."; pur. J. Pharmacol. 349:97-105(1998).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                       STRAIN=Sprague-Dawley;
MEDLINE=96421636; PubMed=8824284;
                                                                                                                                                                                                                                                                                                                                                   Parker E.M., Babij C.K., Balasubramaniam A.,
Hamud F., Mukhopadhyay G., Rudinski M.S., Ta
Mullins D.E., Salisbury B.G.;
"GR231118 (1229U91) and other analogues of t
                                                                                                                                                                                                                           SEQUENCE OF 12-456 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98332165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
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Sciurognathi;
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▼ [11]
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the European Bioinformatics Institute. The
use by non-profit institutions modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U56078; AAC52677.1; -. EMBL; AF044264; AAC15670.1; EMBL; U66274; AAC52845.1; -.
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                                           248
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                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE INVOLVED IN FEEDING DISORDERS. SUBCELLULAR LOCATION: Integral me TISSUE SPECIFICITY: BRAIN; HYPOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO FAMILY 1 CHIGHEST TO TACHYKININS RECEPTORS.
                                                                                                 FHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVC-
                                                                                                                                                                              MGNLLILMAVMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKAMCHI
                                                                                                                                                                                                                                              QDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Eluropean Bioinformatics Institute. There are no rest
                                                                                                                                               MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV
                                                                                                                                                                                        MGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHI
                                                                                                                                                                                                                        QDSSMEFKLEEHFNKTFVTENNTAAARNAAFPAWEDYRGSVDDLQYFLIGLYTFVSLLGF
LPAPAGPSQGKHLAVPENPASVRSQLSPSSKVIPGVPICFEVKPEESSDAHEMRVKRSIT
                                           SISCGLSHKENRLEENEMINLTLQPSKKSRNQAKTPSTQKWSYSFIRKHRRRYSKKTACV
                                                                 ---IRLKRRNNMMDK--
                                                                                      FHSLVELKETFGSALLSSKYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCR
                                                                                                                                   MPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPV
                                                                                                                                                                                                                                                                     304;
                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                      Conservative
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67.9%;
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O FAMILY 1 OF O
                                                                                                                                                                                                                                                                                                                  WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                      21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                     Pred. No. 8.26
1; Mismatches
                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
; 5157ABE341BA707E CRC64;
                                                                                                                                                                                                                                                                                 Score 1536;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FALSE_NEG
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                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                         Length 456;
                                                                -MRDNKYRSS-----
                                                                                                                                                                                                                                                                      Indels 104;
                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sus scrofa gene for neuropeptide Y receptor type 5, complete cds."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson L., Larhammar D.;

"Porcine NPY receptors NPYIR, NPY2R and comparative analysis.";

Submitted /NOV."
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097969;
                         TRANSMEM
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                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                       EMBL; AF106083; AAD13778.1; -.
EMBL; AB019185; BAA34055.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
      DOMAIN
                                                                       TRANSMEM
                                                                                             DOMAIN
                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor).
NPY5R OR NPYR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide Y
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKKRSRSVFYRLTILILVFAVSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLLGMMS
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receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5
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: Lipoprotein;
39 1
62 1
74 C
95 95 E
115 E
1157 3
1157 C
1178 4
210 E
232 5
311 C
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                                                                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                             2 (POTENTIAL).
EXTRACELLULAR (
3 (POTENTIAL)
EXTRACELLULAR
5 (POTENTIAL).
CYTOPLASMIC (P
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CARBOHYD
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                                 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVC-----
                                                                                                                                                                     QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
                NPILYGFLNNGIKADLVSLIHCLHM
                                                                                                   GLSSQDSKLEENEMINLTLQPAKRSGPQAKLSHHPKWTYSFIRRHRRRYSKKTACVRPAP
                                                                                                                                    VELQESFGSAWLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRTISC
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                                                                   AGPALESREGRPPGKVGSMQSQPPPSNKFMPGVPTCFEVKPEENSDVPEMRVSRSIMRLR
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                  Score 1534.5; DB Pred. No. 9.9e-88;
                                                                                                                                                                                                                                                                                                                            6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            PALMITATE (POTENTIAL).
B7F616C2394C6CA0 CRC64;
445
                350
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                                                                                    ----YRS
                                                                                                                                                                                                                                                                           17;
                                                                                                                    IRLKRR----
                                                                                                                                                                                                                                                                                           1; Length 446;
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RESULT 5
NY5R_M
AC 070342
DT 15-DEC
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT Neurop
DE recept
GN NP5R
OS Mus mu
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RA BOTOWE
RA Vaysse
RA Vaysse
RT "Molec
RT Regul.
RN [2]
RP SEQUEN
RA Chen |
                                                        Borowsky B., Walker M.W., Bard J., W
Vaysse P., Branchek T.A., Gerald C.;
"Molecular biology and pharmacology
species homologs.";
Regul. Pept. 75:45-53(1998).
  STRAIN=129/Sv;
Chen H., Adams
                                               Regul.
                                                                                                                                SEQUENCE FROM N.A. MEDLINE=99017379; PubMed=9802393;
                                                                                                                                                                                       Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                              070342: 035380; Q9JMK1;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                SEQUENCE FROM
                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last annotation update)
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5
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                                                                                                                                                                                                                     (Mouse).
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  TISSUE=Brain;
S., McWhinnie
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
    McWhinnie
                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                     Bard J., W
Gerald C.;
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                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
  Bayne M.,
                                                                                                                 Weinshank R.L.,
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    Gadski
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    Zastawny R.;
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Matches 305
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:108082; Npy5r.
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mouse neuropeptide Y Y5 extracellular domain.";
                                                                                                                                                                                         SEQUENCE
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FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENVLATE OF THIS RECEPTOR IS MEDIATED BY G PROTEIN HAT INHIBITS ADENVLATE CYCLASE ACTIVITY. SEEMS TO BE ASSOCIATED WITH FOOD INTAKE. COULD BE INVOLVED IN FEEDING DISORDERS (BY SIMILARITY).

SUBCELLULAR LOCATION: INTEGRAL BY SIMILARITY.

SUBCELLULAR LOCATION: INTEGRAL OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIGHEST TO TACHYKININS RECEPTORS.
LQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTL 109
                                                          MEVKLEEHFNKTFVTENNTAASQNTASPAWEDYRGTENNTSAARNTAFPVWEDYRGSVDD
                                                                                            MDLELDEYYNKTLATENNTAAT - - -
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AB001346;
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L -> F (IN REF. 1).
K -> Q (IN REF. 3).
K -> Q (IN REF. 3).
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CYTOPLASMIC (1
6 (POTENTIAL)
                                                                                                                                        Score 1514.5;
Pred. No. 1.7e
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5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (
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15-JUL-1998
15-DEC-1998
15-JUL-1999
DOMAIN
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                                                                                                                                                                                                                         InterPro;
Pfam; PF00
                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTII-
-i- SUBCELLULAR LOCATION: Integral membrane protein
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN CO
HIGHEST TO TACHYKININS RECEPTORS.
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Mammalia; Eutheria;
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PF00001; 7tm_1; 1.
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CYTOPLASMIC (POTENTIAL).
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(See http://www.isb-sib.ch/announce/
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NPY5R:

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002835;
15-JUL-1998
15-JUL-1999
16-OCT-2001
                                   TISSUE=Hypothalamus; MEDLINE=99017380; PubMed=9802394; Malmstroem R.E., Hoekfelt T., Bjoerkman Ekstrand A.J., Lundberg J.M.; "Characterization and molecular cloning receptor subtypes in pig and dog."; Regul. Pept. 75:55-70(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
DISULFID
LIPID
SEQUENCE
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CARBOHYD
CARBOHYD
 Andersson
          Wraith A.,
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                     Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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DOMAIN
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DOMAIN
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DOMAIN
                   SEQUENCE FROM N.A.
                                                                                                                                                                    Neuropeptide NPY1R.
                                                                                                                              NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                     TKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTCVNP
                                                                                                                                                                                                                                                                                                                                                           CFDKFPSDSHRLSYTTLLMLQYFGPLCFIFICYFKIYIRLKRRNNMMDKMRDNKYRSSE
                                                                                                                                                                                                                                                                                                                                                                               CVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                         VNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCVSITVSIFSLVLIAVERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENSQFLAFESDDCHLPLAMIFTLALAYGAVIILGVTGNLALIMIILKQKEMRNVTNILI
                                                                                                                                                                                                                                                                                                                                       SRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  .
 Tornsten A.,
L., Larhammar
                                                                                                                                                                             (Rel. 36, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
e Y receptor type 1 (NPY1-R).
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 Chardon D.;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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6 (POTENTIAL
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(GLCNAC . . .)

(GLCNAC . . .)
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        Chowdhary
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        В.Р.,
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CARBOHYD
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LIPID
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Pfam; pF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comparative analysis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF005779; AAC26836.1; -. EMBL; AF106081; AAD13776.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                              MMDKMRDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYC
                                                          FQNVTLDAFKDKYVCFDKFLSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRNN
                                                                                                                                          LKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEVMCKLNPFVQCVSIT
                                                                                                                                                     YYNKTLATENNTAATRNSDEPVWDDYKSSVDDLQYFLIGL-YTFVSLLGEMGNLLILMAL
                                                                                                                       VSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVELQET
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                     MMDKMRDNKYRSSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFL
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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N-LINKED (GLCN)
N-LINKED (GLCN)
BY SIMILARITY:
PALMITATE (POTI)
L -> P (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed.
                                                                                                                                                                                                                        Score 650; DB 1;
Pred. No. 1.6e-33
B; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                     7 (POTENTIAL)
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                                                                                           EMBL; M88461; AAA73215.1; -.
EMBL; M84755; AAA59920.1; -.
EMBL; L07614; -; NOT_ANNOTATED_CDS.
EMBL; L07615; AAA59947.1; -.
EMBL; A26481; CAA01819.1; -.
EMBL; A26481; CAA01787.1; -.
EMBL; A26126; CAA01787.1; -.
PIR; A42773; A42773
PIR; A42773; A42773
PIR; A46133; A46133
PIR; A46490; AA5490.
Genew; HGNC:7956; NPYIR.
MIM; 162641; -.
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between
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Herzog H., Baumgartner M., Vivero C., Selbie L.A., Auer B., (Merzog H., Baumgartner M., Vivero C., Selbie L.A., Auer B., (Merzog H., Baumgartner M., Vivero C., Selbie L.A., Auer B., (Merzog Herzog He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herzog H., Hort Y.J., Ball H.J., Hayes G., Shine "Cloned human neuropeptide Y receptor couples to messenger systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92283782; PubMed-1317848;
Larhanmar D., Blomqvist A.G., Yee F.
Wahlestedt C.R.;
"Cloning and functional expression o
YY receptor of the Y1 type.";
D. Biol. Chem. 267:10935-10938(1992)
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropeptide Y receptor type 1 (NPY1-R).
NPY1R OR NPYR OR NPYY1.
  InterPro; IPR000276; GPCR_Rhodpsn. Pfam; pF00001; 7tm_1; 1. PRIWTS; PR00237; GPCRRHODOSN. PROSITE; PS00237; G_PROTEIN_RECEP
                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The By non-profit institutions as long
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES NPY > [PRO-34] PYY, PYY AND [LEU-31, PRO-34] NPY > NPY (2-36) > [ILE-31, GLN-34] PP AND PYY (3-36) > PP > NPY FREE ACID. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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G_PROTEIN_RECEP_F1_1;
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CARBOHYD
SEQUENCE FROM N.A.

MEDLINE=99427767; PubMed=10499421;
Berglund M.M., Holmberg S.K.S., Eri
Serradeil-Le Gal C., Chhajiani V.,
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                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                       NCBI_TaxID=10141;
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BY SIMILARITY.
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Hystricognathi; Caviidae; Cavia.
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Peptides 20:1043-1053(1999).
-!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO TACHYKININS RECEPTORS.
WNHQIIATCNHNLLFLLCHLTAMISTCVNPIFYGFLNKNFQRDL
                                                                                                                     FNDNLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADL
                                                                                                                                                                                        ASSLPFMIYQVLTDEPFQNVTLDAFKDKLVCFDQFPSDSHRLSYTTLLLVLQYFGPLCFI
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7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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PALMITATE (POTENTIAL).
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CARBOHYD
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-!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST TO TACHYKININS RECEPTORS.
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Pfam; PF00001; 7tm_1; 1.
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YNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGL-YTFVSLLGFMGNLLILMALM
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                                                                                                                                                                                    366 AA;
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(Rel. 28, Last sequence updated)
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(Rel. 37, Last annotation updated)
                                                                Conservative
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. .) (F

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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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Pred. No. 9.
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9A603FC67 CRC64;
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RESULT 11
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   modified
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                                                                                                                                                                                                                                                                                                                                                                                      "Identification of two isoforms of mouse neuropeptide Y-Y1 receptor generated by alternative splicing. Isolation, genomic structure, and functional expression of the receptors.";
J. Biol. Chem. 270:30102-30110(1995).
-i- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NY1R_MOUSE STANDARD: PRT; 382 AA. Q04573; Q61993; Q1-OCT-1993 (Rel. 27, Created) 01-OCT-1993 (Rel. 27, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) weuropeptide Y receptor type 1 (NPY1-R).
                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific expression.";
FEBS Lett. 314:285-288(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93106169: PubMed-1468559;
Eva C., Oberto A., Sprengel R., Genazzani E.;
"The murine NPY-1 receptor gene. Structure and delineation of tissue-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96102072; PubMed-8530415;
Nakamura M., Sakanaka C., Aoki Y., Ogasawara H.,
Nakamura H., Matsumoto T., Shimizu T., Noma M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                       between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . musculus (Mouse).
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                             s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                   DEVELOPMENTAL STAGE: THE BETA FORM IS EXPRESSED IN EMBRYONIC DEVELOPMENTAL STAGE (7 AND 11 DAYS). THE BETA FORM IS AN EMBRYO AND A BONE MARROW FORM OF NPI-R, WHICH DECREASES IN THE EXPRESSION DURING DEVELOPMENT AND DIFFERENTIATION.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; NPY1-R ALTERNATIVE SPLICING.

NPY1-R BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: THE ALPHA FORM IS HIGHLY EXPRESSED IN THE BRAIN, HEART, KIDNEY, SPLEEN, SKELETAL MUSCLE, AND LUNG, WHEREAS THE BETA RECEPTOR MRNA WAS NOT DETECTED IN THESE TISSUES. HOWEVER, THE BETA FORM IS EXPRESSED IN MOUSE EMBRYONIC DEVELOPMENTAL STAGE (7 AND 11 DAYS), BONE MARROW CELLS AND SEVERAL HEMATOPOIETIC CELL
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 non-profit institutions as long and this statement is not removed. requires a license agreement (See
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  (See http://www.isb-sib.ch/announce/
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                                                                         a collaboration
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Best Local
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SEQUENCE
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CARBOHYD
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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Pfam; PF00001; 7tm_1; 1.
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                                                           IRLKRRNNMMDKMRDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISN 305
                                                                                                                                               ILTD--EPFQNVSLAAFKDKYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIY
                                                                                                                                                                                                                    FLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFH 188
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                                                CNHNLLFLLCHLTAMISTCVNPIFYGFLNKNFQRDL 330
                                                                                                                                                                       SLVELQETFGSALLSS---RYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVC
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37.8%;
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3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (F
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Pred. No. 1.7e-
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MISSING (IN ISOFORM NPY1-R BETA).
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N-LINKED (GLCNAC. . .)
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7 (POTENTIAL)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY
-i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91032093; PubMed=2172008; Eva C., Keinaenen K., Monyer H., Seeburg P.H., Seburg rocoupled molecular cloning of a novel G protein-coupled belong to the neuropeptide receptor family."; FEBS Lett. 271:81-84(1990).
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Pfam; PF00001; 7tm_1; 1.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: BRAIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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een the Swiss Institute of Bioinformatics and the EN
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(Rel. 39, Last annotation update)
e Y receptor type 1 (NPY1-R) (FC5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                       MW.
                                                                                71;
                                                                                                                                                                                                                                                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
PALMITATE (POTENTIAL).
                                                                                Score 633.5;
Pred. No. 1.7e
71; Mismatches
                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC
2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                  1D6AA038065C07C3 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                     No. 1.7
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                                                                                                     .7e-32;
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                          DB
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                                                                                                                                                                  CRC64;
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                                                                                                                      Length
                                                                                  Indels
                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                  6,
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                                                                                Gaps
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RESULT 13
NY6R_RABIT
                    DOMAIN
                                        TRANSMEM
                                                                                TRANSMEM
                                                                                                                     Phosphorylation;
                                                                                                                                     PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; G-protein coupled receptor; Transmembrar
                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                            entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H., Togami J., Kimura Y., Okada M., Yamaguchi T.; "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in
                                                            DOMAIN
                                                                                                  DOMAIN
                                                                                                                                                                                                                                                          EMBL; D86521; BAA13104.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primate species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Japanese white; TISSUE=Skeletal MEDLINE=97066888; PubMed=8910290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Łuc
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P79217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuropeptide
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30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NY6R_RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO FAMILY 1 OF G-PRO HIGHEST TO TACHYKININS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Siol. Chem. 271:2721
FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYCLASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF THIS RECEPTOR IS MEDIATED BY G PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILYGFLNNGIKADL 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSR
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                                                                                                                                                                                               PR00237; GPCRRHODOPSN
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35
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70
91
111
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(Rel. 36, Last sequence upda
(Rel. 39, Last annotation up
Y receptor type 6 (NPY6-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271:27217-27220(1996)
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: Lipoprotein;
34 E
57 C
69 C
110 E
132 3
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Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR NEUROPEPTIDE Y AND PEPTIDE YY.
                                                                                                                                     Transmembrane;
2 (POTENTIAL).
EXTRACELLULAR
3 (POTENTIAL).
                                                        1 (POTENTIAL)
CYTOPLASMIC (
                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                     Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle;
                                                                                                                                                                                                                                                                                                                                                 There are no restrictions in as its content is in
                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THAT
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                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
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commercial
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Вþ Qγ Вb QУ 밁 Qy DЬ Qy

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NY6R_MOUSE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q61212;
01-NOV-1997
01-NOV-1997
30-MAY-2000
                                                                                                            Weinberg D.H., Sirinathsinghji D.J.S., Tan C.P., Shiao L. Morin N., Rigby M.R., Heavens R.H., Rapoport D.R., Bayne Cascieri M.A., Strader C.D., Linemeyer D.L., Macneil D.J. "Cloning and expression of a novel neuropeptide Y recepto J. Biol. Chem. 271:16435-16438(1996).
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Neuropeptide Y receptor type 6 (NPY6-R) (Pancreatic receptor 2) (PP2).
NPY6R OR PPYRZ OR NPY5R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
CARBOHYD
MEDLINE-97066971; PubMed-8910373; Gregor P., Feng Y., Decarr L.B.,
                                             SEQUENCE FROM N.A.
STRAIN=129/SV;
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NY6R_MOUSE
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                      MEDLINE=96279200; PubMed=8663568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLTD--EPFRNLSLPTDLYSHHVVCVEHWPSKTNQLLYSTSLIMLQYFVPLGFMFICYLK
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Pfam; pF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor and its J. Biol. Chem. 27-1- FUNCTION: REC
                                                                                                                                                                                                                    LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                       SEQUENCE
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TISSUE SPECIFICITY: KIDNEY AND DISCRETE REGIONS OF THE
HYPOTHALAMUS INCLUDING THE SUPRACHIASMATIC NUCLEUS, AN'
HYPOTHALAMUS, BED NUCLEUS STRIA TERMINALIS, AND THE VEH
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European Bioinformatics Institute.
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IFSLVLIAIERYQLIVNPRGWKPRVAHAYWGIILIWLISLTLSIPLFLSYHLTNEPFHNL
                        TLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPL-----PVFHSL
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                                                 QREAQNVTNILIANLSLSDILVCVMCIPFTVIYTLMDHWVFGNTMCKLTSYVQSVSVSVS
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CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

LINKED (GLCNAC. . .) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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E4AABB987CEB74B7 CRC64;
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No. 1.5e-27;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differences
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salaneck E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D. "Chicken neuropeptide Y receptor Y2: structural and pharmacological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-20532533; PubMed-11078884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Copyright (c) 1993 - 2002 Compugen
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hypothetical prote
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cholecystokinin ty
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Gene: GDB:NPYIR; NPYR Cross-references: GDB:132643; OMIM:162641 Map position: 4q31.3-4q32 Superfamily: neurokinin 1 receptor Keywords: appetite; G protein coupled receptor; glycoprotein; lipop 37-66/Domain: transmembrane #status predicted <tm1> 77-103/Domain: transmembrane #status predicted <tm2> 118-136/Jomain: transmembrane #status predicted <tm4> 209-232/Domain: transmembrane #status predicted <tm4> 209-232/Domain: transmembrane #status predicted <tm5> 261-286/Jomain: transmembrane #status predicted <tm6> 300-323/Domain: transmembrane #status predicted <tm7> 113-198/Disulfide bonds: #status predicted <tm7></tm7></tm7></tm7></tm7></tm7></tm7></tm6></tm5></tm4></tm4></tm2></tm1>	A45490 A45490 A45490 C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: A45490; A4613; A42773 R; Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Sh J, Biol. Chem. 286, 6703-6707, 1993 A; Title: Genomic organization, localization, and allelic differences A; Reference number: A45490; MUID:93203272; PMID:8095935 A; Accession: A45490 A; Molecule type: DNA A; Residues: 1-384 <her> A; Cross references: GB:L07615; NID:g189284; PIDN:AAA59947.1; PID:g189; A; Cross references: GB:L07615; NID:g189284; PIDN:AAA59947.1; PID:g189; A; Cross references: GB:L07615; NID:g189284; PIDN:AAA59947.1; PID:g189; A; Mote: sequence extracted from NCBI backbone (NCBIN:128005, NCBIP:128, NCBI</her>	30 332 18.1 457 2 T29741 31 327.5 17.8 384 1 S00516 neurokinin 32 324 17.6 402 2 156595 neurokinin 33 323 17.6 374 2 T19340 cholecysto. 34 322 17.5 452 2 A46195 35 321.5 17.5 491 2 C404790 glucocorti, 36 321 17.5 390 2 B88684 protein AC 37 320 17.4 416 2 T39946 protein AC 38 317 17.3 394 2 157957 neurokinin 39 316.5 17.0 384 2 S20303 41 312.5 17.0 384 2 S20303 42 312. 17.0 384 2 S20304 43 311.5 17.0 384 2 S20304 44 311 16.9 453 2 S32817 45 310.5 16.9 376 2 T19186 hypothetic.
tein; li predicte	change 20-A Auer, B.; S differences differences 1; PID:918 05, NCBIP:1 .; Selble, two differe lation 38) , H.; Wahle ropeptide Y ropeptide Y	hypothetical prote neurokinin 2 recep neurokinin 2 recep hypothetical prote cholecystokinin B glucocorticoid in B glucocorticoid in B glucocorticoid in protein AC7.1 [imp hypothetical prote neurokinin 2 recep hypothetical prote neurokinin 2 recep tachykinin recepto gastrin recepsor gastrin receptor sypothetical prote neurokinin 1 recep gastrin receptor systems are supported that the systems are supported that the systems are supported to the systems are systems are supported to the systems are systems are systems.

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A;Title: Cloning and sequence analysis of a neuropeptide Y/pept A;Reference number: S55924; MUID:95260870; PMID:7742373
A;Accession: S55924
A;Status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:L25416; NID:g409169
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
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S71152
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A; Residues: 1-278, 'T', 280-366 <BLO>
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A;Description: Cloning and sequencing of an neuropeptide Y/peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuropeptide Y/peptide YY receptor Y1 - African clawed frog C;Species: Xenopus Laevis (African clawed frog) C;Date: 27-Oct-196 #sequence_revision 13-Mar-1997 #text_change C;Accession: S71152; S55924
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     GSALLSS----RYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNM
                                                          SIFSLVLIAIERHQLIINPRGWRPNNRHACFGITVIWGFAMACSTPLMMYSVLTD--EPF
                                                                                                         STLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVELQETF
                                                                                                                                                                                                       KKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLV 137
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                                                                                                                                                                KQKEMRNVTNILIVNLSFSDLLATIMCLPFTLIYTLMDHWIFGEVMCKLNEYIQCVSVTV
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R;Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
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A; Residues: 1-349 <EVA>
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;Species: Rattus norvegicus (Norway
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CNHNLLFLLCHLTAMISTCVNPIFYGFLNKNFQRDL
                              RHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADL 341
                                                                                                                                  IRLKRRNNMMDKMRDNKYRSSRSRSVEYRLTILILVFAVSWMPLHLFHVVTDFNDNLISN
                                                                                                                                                                                                                                                                 SLVELQETFGSALLSS----RYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVC
                                                                                                                                                                                                                                                                                                                FVQCVSITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQ
                                                                                                         IRLKRRNNMMDKIRDSKYRSSETKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72;
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2; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 633.5; DB 2
Pred. No. 4.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transduction Properties
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330
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F;114-135/Domain: transmembrane #status predicted <TM3> F;155-175/Domain: transmembrane #status predicted <TM4> F;215-231/Domain: transmembrane #status predicted <TM5> F;262-285/Domain: transmembrane #status predicted <TM6> F;262-285/Domain: transmembrane #status predicted <TM6> F;299-322/Domain: transmembrane #status predicted <TM7> F;2,11,17/Binding site: carbohydrate (Asn) (covalent) #status F;346/Binding site: phosphate (Thr) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Rosidues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNEKI' <KRA>
A;Cross-references: EMBL:211504; NID:g57636; PIDN:CAA77579.1; PID:
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprote
F;39-61/Domain: transmembrane #status predicted <TM1>
F;73-93/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
C;Accession: S12863; S19101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Molecular cloning of a novel G protein-coupled receptor that may belong A; Reference number: S12863; MUID:91032093; PMID:2172008
20 NKTL--ATENNTA---ATRNSDFPVWDDYKSSVDDLQYFLIGLYTF-----VSLLGFMG
                                                                                                                                                                                                                               NSTLFSRVENYSVHYNVSENSPFLAFEN----DDCHLPLAVIFTLALAYGAVIILGVSG
                                                                                              NLALIIIILKQKEMRNVTNILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNP
                                                                                                                                                           NLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monyer, H.; Seeburg, P.; Sprengel,
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neuropeptide Y/peptide YY receptor Y1 - mouse
C:Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: B46133
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second A;Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: B46133
                                                                                                                                                              A:Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-382 <HER>
A:Note: sequence extracted from NCBI backbone (NCBIP:108539) C;Superfamily: neurokinin 1 receptor C;Keywords: appetite; G protein-coupled receptor; transmembrane
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A;Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific A;Reference number: S27388; MUID:93106169; PMID:1468559
A;Accession: S27388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-382 <EVA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                       Query Match
                                                                                                                                                            Keywords: appetite; G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                     Local Similarity
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    SENSPELAFENDDCHLPLAVIFTLALAYGAVIILGVSGNLALIIIILKQKEMRNVTNILI
                                           TRNSDFPVWDDYKSSVDDLQYFLIGL-YTFVSLLGFMGNLLILMALMKKRNQKTTVNFLI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADL: |:: :|| | :| |:|| | | || || : || |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLVELQETFGSALLSS----RYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRLKRRNNMMDKIRDSKYRSSETKRINIMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIAT
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                                                                                                   34.5%;
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                                                                                Score 633.5; DB 2;
Pred. No. 4.5e-44;
1; Mismatches 116;
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3; Mismatches
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neuropeptide Y/peptide YY receptor Y4 - C;Species: Homo sapiens (man) C;Date: 01-Mar-1996 #sequence_revision (
                                                             RESULT
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C;Accession: S63685
R;Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J. FEBS Lett. 381, 58-62, 1996
A;Title: Cloning and characterization of a novel receptor to pancreatic polypeptide A;Reference number: S63685; MUID:96193913; PMID:8641440
A;Accession: S63685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuropeptide Y receptor D type - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
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S63685
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                                                                                                                                            278 LILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGI 337
                                                                                                                                                                                                                                                                                                 159 GIVVIWFISCFLSLPFLANSTLNDLFHYNHSKVVE-----FLEDKVVCFVSWSSDHH 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                          KADLVSLI---HC
                                                                                                                                                                                                 RLIYTTFLLLFQYCIPLAFILVCYIRIYQRLQRQKHVFHAHACSS-RAGQMKRINSMLMT
                                                                                                                                                                                                                                               RIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSRSVFYRLTI 277
                                                                                                                                                                                                                                                                                                                              LIATVWTLGFAICSPL------PVFH----SLVELQETFGSALLSSRYLCVESWPSDSY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLAFITTYSIETILGVLGNLCLIFVTTRQKEKSNVTNLLIANLAFSDFLMCLICQPLT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSR
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KKDIKALVLTCHC
                                                                                               MVTAFAVLWLPLHVFNTLEDWYQEAIPACHGNLIFLMCHLLAMASTCVNPFIYGFLNINF
                                                                                                                                                                                                                                                                                                                                                                                                   VTYTIMDYWIFGEVLCKMLTFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSIFQAYL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF 16E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKRINVMLLSIVVAFAVCWLPLTIFNTVFDWNHQIIATCNHNLLFLLCHLTAMISTCVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIRLKRRNNMMDKIRDSKYRSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTD--EPFQNVSLAAFKDKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVELQETFGSALLSS---RYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                               347
342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 515.5; DB 2; 32.9%; Pred. No. 1.7e-34; tive 68; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 375;
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A; Accession: G02300
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Yan, H.; Yang, J.; Marasco, submitted to the EMBL Data Lil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreatic polypeptide receptor - human
C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                            C; Superfamily: neurokinin
                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: U42387; NID: g1314327; PIDN: AAB07759.1;
                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDB.
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R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.
J. Biol. Chem. 270, 26762-26765, 1995
A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic A;Reference number: I39182; MUID:96070761; PMID:7592911
A;Accession: I39182
                                                                                                                                                                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-375 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross_references: EMBL:U35232; NID:g1063629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                          Query Match
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   159
                                       169
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                                                                               99
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                                                                                                                                                                         49 DLQYFLIGLYTFVSLLGEMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFT | | | | | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                      Local
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GIVLIWVIACVLSLPF-LANSILENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTF
                                   LIATVWTLGFAICSPLPVFHSLVE--LQETFGSAL--LSSRYLCVESWPSDSYRIAFTIS
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                                                                         SVYTIMDYWIFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYL
                                                                                                           LTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF 168
                                                                                                                                                     DVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLVQYILPLVCLTVSHTSVCIRLKRRNNMMDKMRDNKYRSSRSRSVFYRLTILILVFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIVLIWVIACVLSLPF-LANSILENVFHKNHSKALEFLADKVVCTESWPLAHHRTIYTTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLFQYCLPLGFILVCYARIYRRLQRQGRVFHK-GTYSLRAGHMKQVNVVLVVMVVAFAV
                                                                                                                                                                                                                                                                                                                                                  1-375 <YAN>
                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                              28.0%; score 514; DB 2; I
32.9%; Pred. No. 2.3e-34;
tive 72; Mismatches 124;
                                                                                                                                                                                                                                                                                                            1 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                             J.; Yamaguchi, K.; Brenner,
brary, December 1995
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Pred.
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No. 1.9e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124;
                                                                                                                                                                                                                                                                    Length 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.; Collins,
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                                   224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.; Karbon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C:Accession: I39187: I39187:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;269-291/Domain: transmembrane *status predicted F;305-328/Domain: transmembrane *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;166-186/Domain: transmembrane #status predicted <TM4>F;221-237/Domain: transmembrane #status predicted <TM5>F;221-291/Domain: transmembrane #status predicted <TM5>F;269-291/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-171, 'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U36269; NID:g1063633; PIDN:AAC50281.1; PID:g1063634 R;Rose, P.M.; Fernandes, P.: Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Koduk J. Biol. Chem. 270, 22661-22664, 19564. Sittle: Cloning and functional expression of a cDNA encoding a human type 2 A;Reference number: I39163; MUID:96032678; PMID:7559383 A;Accession: I39163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Gerald, C.; Walker, M.W.; Vaysse, P.J.
J. BLO1. Chem. 270, 26758-26761, 1995
A;Title: Expression cloning and pharmacological characterization
A;Reference number: 139187; MUID:96070760; PMID:7592910
A;Accession: 139187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;49-76/Domain: transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 4q31-4q31
C:Superfamily: neurokinin 1 receptor
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A; Accession: G02301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-133, 'A', 135-381 < ROS>
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neuropeptide Y/peptide YY receptor Y2 - human
neuropeptide Y/peptide YY receptor
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A; Residues: 1-381 <GER>
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109 LTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYF

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RESULT 10
152315
G protein-coupled receptor UHR-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: 152315
R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A;Title: Sequence and tissue distribution of a candidate G-coupl
A;Reference number: 152315; MUID:95251659; PMID:7733930
A;Accession: 152315
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)
N;Alternate names: G protein-coupled receptor PR4
C;Speciles: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
C;Accession: A41738
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.
                                                                                                       RESULT 11
A41738
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A;Molecule type: mRNA
A;Residues: 1-370 <RES-
A;Cross-references: GB:S77867; NID:g998527;
C;Superfamily: neurokinin 1 receptor
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                                                                                                                                                                                                                                                                                                                                            LLSSRYLCVESWPS-DSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRR----NNMMD 256
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                                                                                                                                                                          WLAMSSACYNPFIYAWLHDSFREELRKML
                                                                                                                                                                                                                                                                                                                 --HDVRLCEEFWGSQERQRQIYAWGLLLGTYLLPLLAILLSYVRVSVKLRNRVVPGSVTQ
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                                                                                                                                                                                                           LLGMMSCCLNPILYGFLNNGIKADLVSLI
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31.6%; Pred. No. 1.9e ...
*+ive 71; Mismatches 137;
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J. Biol. Chem. 267, 9-12, 1992
A;Title: Cloning, functional expression, and developmental regulation of a A;Reference number: A41738; MUID:92112730; PMID:1370455
A;Recession: A41738
A;Molecule type: mRNA
A;Residues: 1-449 < LIA>
A;Residues: 1-449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: The sequence of C. elegans cosmid C:
A;Reference number: Z18378
A;Reference number: Z18378
A;Accession: T156/2
A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C25G6.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Deceies: Co-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T15622
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A;Cross-references: FlyBase:FBgn0004842
C;Superfamily: neurokinin l receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 37/3; 87/3; 137/2; 203/3; C; Superfamily: neurokinin 1 receptor
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C;Genetics:
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A; Residues: 1-455 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:C25G6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 DDYKSSYDDL---QYFLI---GLYTFYSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                               SVDDLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANH 165
                                                                                                                                      SPKEFGYFITFAYMLIILFGAIGNFLTIIVVILNPAMRTTRNFFILNLALSDFFVCIVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HWLAMSHCCYNPIIYCYMNARFRSGFVQLMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHF------KLVYCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHPISNNLTANHGYFLIATVWTLGFAICSPLPV-----FHSLVELQETFGSALLS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSDILVVLFCSPFTLTSV-LLDQWMFGKVMCHIMPFLQCVSVLVSTLILISIAIVRYHMI 153
PTTLYTVLYMFWPFSRTLCKIAGSLQGFNIFLSTFSIASIAVDRYVLIIFPTKRERQQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMARSKRKMVKMMLTV-VIVFTCCWLPFNILQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KYICREMWPSRSQEYYYTLSLFALQFVVPLGVLIFTYARITIRVWAKRPPGEAETNRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               37/3; 87/3; 137/2; 203/3; 260/2; 292/3; 346/2; 402/2
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                  21.7%; Score 397.5; DB 2 30.8%; Pred. No. 8.4e-25;
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29.6%; Pred. No. 9.2e-27;
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                                                                                                                                                                                                                                                                                    Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                               Length 455;
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RESULT 13
B40470
glucocorticoid-induced receptor precursor, short form RP23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C;Accession: B40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-ce.
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: B40470
A;Accession: B40470
hypothetical protein F41E7.3 - Caenorhabditis elegans c; Specles: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C; Accession: T22076 R; Lennard, N. submitted to the EMBL Data Library, November 1995 A; Reference number: Z19509
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A; Residues: 1-423 <HAR>
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                                                                                                                                                                                                                       MMSCCLNPILYGFLNNGIKADLVSLI 345
                                                                                                                                                                                                                                                                                          RSSRSRSVFYRLTILILV-FAVSWMPLHLFHVVTDFNDNLISNRHF---KLVYCICHLLG
                                                                                                                                                                                                                                                                                                                          SLCLPDFPEPADLFWKYLDLATFILLYLLPLFIISVAYARVAKKLWLCNTIGDVTTEQYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLILISI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYTESDWQNEVGRRRYGAESQNPTVKALLIVAYSFTIVESLEGNVLVCHVIFKNQRMHSA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISKGTYTLAVLITQYAFPLFSLVFAYSRIAHRMKLRFANRNQNVTTNTNTSQRRRSVVE
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                                                                 15-Oct-1999 #text_change
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A;Map position: X
A;Introns: 76/2; 161/3; 22
C;Superfamily: neurokinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-412 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T22076
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                                                                                                                                                                                                                                                                                                   LIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCV-----
RGYFSFVFLSVHLMSMTATAWNPILYAFMNETFREEFAKVVPCL
                                                                                                                                                                                                                                                                                                                                                EMEYFRPFFISMYCAVFLVASSGNFLVSNIIFDFSSFPTTVFKVVYVVMTNKRMQTITNI 61
                                                                                                                                                                                                                                                                                                                                                                                 DLQY---FLIGLYTFVSLLGFMGNLL-----
                                NRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADLVSLIHCL 348
                                                                    WLFLNSRQSMTERKSDIK----RKKRLLRMLIVMVVIFAICWFPFNLLNCLRDLKLDNFM
                                                                                                 CIRLKRRNNMMDKMRDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLIS
                                                                                                                                                                                                                                         ----SVLVSTLILISIAIVRYHMIKHPISN----NLTANHGYFLIATVWTLGFAICSPL
                                                                                                                                                                                                                                                                             FITNLAVSDIMVNFTSLWLTPTYTSIGHWIFGGGLCHGLPLFQGIGLHIDGKLSSDQASN 121
                                                                                                                                                                      PVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSV
                                                                                                                                                                                                         YTGTSIFISTWTLTAIAIDRYIVIVHNSSNININDRMSMRSCLSFIVLIWLCSLLLVTPY
                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220/3; 279/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%;
25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    64;
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Pred.
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335
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JC5599

JC5599

C:Species: Mus musculus (house mouse)
C:Date: 23-Sep-1997 #sequence_revision
C:Accession: JC5599
                                                                                                                                                                                                                                                                                       A;Note: translation not complete C;Comment: This receptor belongs to the seven transmembrane G-protein coupled recepto dder contraction, and cholecystokinin inhibition of food intake. C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, Biochem. Biophys. Res. Commun. 236, 630-635, 1997
A;Title: Molecular structure of the mouse CCK-A receptor gene.
                                                                                                                                                                                                                                                                      F;42-67/Domain:
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-436 <LAC>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: JC5599; MUID: 97396148; PMID: 9245702
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC5599
                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                  LATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNLLILMALMKKRNQ
                                       KTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFLQCVSVLVSTLIL 142
RTVTNIFLLSLAVSDLMLCLFCMPFNLIPNLLKDFIFGSAVCKTTTYFMGTSVSVSTFNL
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                         transmembrane #status predicted <TMM>
                                                                                                                                                                              Conservative
                                                                                                                                                                                                   19.58;
                                                                                                                                                                              78;
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Pred. No. 1.2e
78; Mismatches
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                                                                                        LYSFIFLLSVLGNTLVITVLIRNKRM
                                                                                                                                                                              1.2e-21;
hes 138;
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Db	Qy	ф	Qy	Db	QΥ	рь	δδ	Ъ	Qy
366	318	309	268	249	253	193	201	133	143
366 LSYTSSCVNPIIYCEMNKRERLGEMATEPC 395	318 LGMMSCCLNPILYGFLNNGIKADLVSLIHC 347	309 SAANLIAKKRVIRMLIVIVVLEFLCWMPIFSANAWRAY-DTVSAEKHLSGTPISFILL 365	268 SRSVFYRLTILILVFAVSWMPLHLEHVVTDFNDNLISNRHFKLVYCICHL 317	249 SAKEKRLSSGGGGGGSSSSRYEDSDGCYLQKSRPPRKLELQQLSTSSSGGRINRIRSSG 308	253 NMMDKMRDNKYRSSR 267	193 ANMCRELLPSDAMQQSWQTELLLILELIPGVVMVVAYGLISLELYQGIKFDASQKK 248	LLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCIRLKRRN 252	133 VAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIYSNLVPFTKNNNQT 192	143 ISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSLVELQETFGSA 200

Search completed: November 22, 2002, 13:10:52 Job time : 23 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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 Score
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                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/TCGT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2002 Compugen
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US-09-771-956-33

US-09-771-956-33

US-09-771-956-25

US-09-771-956-25

US-09-771-956-25

US-09-771-956-24

US-09-771-956-24

US-09-771-956-2

US-09-771-956-2

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US-09-962-646-6

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        Sequence 6, Appli
Sequence 10, Appl
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Sequence 21, Appl
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378. 37 366. 366.		326 326	US-10-067-477-1 US-09-804-551B- US-09-292-973-4 US-09-292-973-1 US-09-292-973-2	1, Appli 2, Appl 4, Appl 19, Appl 19, Appl
357. 357. 33		31 31 31 27 23	US-09-826-508-2 US-09-899-532-2 US-09-730-931-2 US-10-044-592-7	22, App 2, Appl 2, Appl 2, Appl 72, App
3334 222		23	US-10-044-592-7 US-10-044-592-7 US-10-077-874-2 US-09-828-538-1	71, App 71, App 2, Appl
32 32 31 317.		25 72 89	-09-828-538- -09-961-848- -10-077-874- -09-828-538-	NONN
			ALIGNMENTS .	
-09-771-956-6 -09-771-956-6 Sequence 6, Application of the patent No. US200100314 Sequence 6, Applicantion of the patent No. US200100314 APPLICANT: Bennett, APPLICANT: Brodbeck, APPLICANT: Krause, J. TITLE OF INVENTION: FILLE OF INVENTION: USENTION NOTE: NOTE: NOTE: NOTE: SOFTWARE: Patentin V. SEQ ID NO 6 LENGTH: 350 TYPE: PRT ORGANISM: Artificial FEATURE: OTHER INFORMATION: D-09-771-956-6	pplication of the pplication o	74A1 774A1 774A1 Michele Robbin ames Chimeri 0,001 0,001 0MBER: 2001-0 31 er: 2.11	771956 C Neuropeptide Y Receptors US/09/771,956 1-29 ce ce	5/Y1 CHIMERA
Query Match Best Local Simi Matches 350;	ilarity Conserv	100.0 100.0 ative	<pre>%; Score 1836; DB 10; Leng %; Pred. No. 8.1e-149; 0; Mismatches 0; Indel</pre>	gth 350; ls 0; Gaps 0;
1 MSFYSK 1 1 MSFYSK 61 VSLLGF 	KQDYNMDLE KQDYNMDLE FMGNLLILM 	LDEYN LDEYN LDEYN ALMKH	NKTLATENNTAATRNSDEPVWDDYKSSVDDLQXIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LQYFLIGLYTF 60 CQYFLIGLYTF 60 CQYFLIGLYTF 120 TSVLLDQWMFG 120
x – x	MPFLQCVS	VLVSTLI	.ILISIAIVRYHMIKHPISNNLTANHGYFL 	18
181 CSPLPV	FHSLVELQ	ETFGSAL	SPLPVFHSLVELOETEGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 	YILPLVCLTVS 240

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US-09-771-956-10
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                                                                                                                             Sequence 20, Application US/09771956 Patent No. US20010031474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 10
LENGTH: 394
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide
FILE REFERENCE: NOUMBER: US/09/771,956
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Krause, James TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ. ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
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mes 339; Conserv
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                                                                                                                                                                                                                                                                            NLISNRHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADL 341
                                                                                                                                                                                                                                                                                                                           HTSVCIRLKRRNNMMDKMRDNKYRSSRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFND 300
                                                                                                                                                                                                                                                                                                                                                                          CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
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                                                                                                                                                                                                                                                                                                          HTSVCIRLKRRNNMMDKMRDNKYRSSRSVFYRLTILILVFAVSWMPLHLFHVVTDFND
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                                                               Chimeric Neuropeptide
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Pred. No. 9.4e-144;
1; Mismatches 1;
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US-09-771-956-26
Sequence 26, Application US/09771956
Patent No. US20010031474A1
                                                                                                                                                                                                                                                                                            NUMBER: PATE

; SOFTWARE: PATE

; SEQ ID NO 26

* FRIGTH: 341
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; OTHER INFORMATION:
US-09-771-956-20
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APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
                                                                                                                                                                         Query Match
Best Local
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Best Local Similarity
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SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide
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                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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                                                                                                        92.5%;
Local Similarity 94.1%;
nes 320; Conservation
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                                                                                           1 MDLELQDFYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60
                           VYCICHLLGMMSCCLNPILYGELNNGIKADLVSLIHCLHM 350
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QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 190
                                                            LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 130
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97.6%;
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Pred. No. 3.3e-137;
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Pred. No. 6.1e-141;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEO ID NOS: 31
SOFTMARE: Patentin Ver. 2.1
SEO ID NO 21
LENGTH: 383
                                                    RESULT 6
US-09-771-956-23
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Sequence 23, Application US/09771956
Patent No. US20010031474A1
GENERAL INFORMATION:
APPLICANT: Bennett, Michele
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Best Local S
Matches 323
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les 323; Conserv
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4; Mismatches
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.2e-136;
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; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo s
US-09-771-956-13
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US-09-771-956-13
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                                                      Best Loc
Matches
                                                                                                                                                               SOFTWARE: SEQ ID NO 13
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                   Query Match
Best Local :
                                                                                                                                                                                      APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y
FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001.01-29
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09771956 Patent No. US20010031474A1
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SEQ ID NO 23
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
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APPLICANT:
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TYPE: PRT
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                                                                    Similarity
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73.2%;
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                                                      Score 1668.5;
Pred. No. 1.8e
6; Mismatches
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/200,673
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 08/566,096
PRIOR APPLICATION NUMBER: 08/566,096
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/349,025
PRIOR APPLICATION NUMBER: 08/349,025
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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US-09-962-646-4
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Patent No. US20020103123A1
GENERAL INFORMATION:
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                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                               SEQ ID NO 4
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TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECER
FILE REFERENCE: 1795/46166BZA
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73.28;
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Pred. No. 1.8e-134;
6; Mismatches 11;
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bennett, ratural APPLICANT: Brodbeck, Robbin APPLICANT: Krause, James TITLE OF INVENTION: Chimeric Neuropeptide TITLE OF INVENTION: Chimeric Neuropeptide PREFERCE: N2000.001
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Best Local
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73.0%;
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Pred. No. 3.2e-134;
7; Mismatches 11;
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GENERAL INFORMATION:

APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y |
FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 395
TYPE: PRT
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US-09-771-956-25
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH.
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Best Local :
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APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide
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ORGANISM: Artificial Sequence
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US-09-771-956-9
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Best Local Sim
Matches 308;
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SEQ ID NO 9
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Best Local S
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APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                LENGTH: 499
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                7 QDYNMDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGF 66
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                                                                                       VSLLGFMGNLLILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQMMFG 120
                                           KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNULTANHGYFLIATVWTLGFAI 180
CSPLPVFHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS
                             KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
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Pred. No. 7.2e-132;
L5; Mismatches 9;
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Pred. No. 2e-129;
7; Mismatches 1
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APPLICANT: WEINSHA
APPLICANT: WALKER,
APPLICANT: BRANCHE
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PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/200,673
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 08/566,096
PRIOR FILING DATE: 1995-12-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEFFILE REFERENCE: 1795/46166BZA
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TYPE: PRT
ORGANISM: Rattus No.
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                                                                                                                                                                                                                                                                                           Conservative
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; OTHER INFORMATION:
US-09-771-956-24
RESULT 15
US-09-771-956-22
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APPLICANT: Bennett, Michel
APPLICANT: Brodbeck, Robbi
APPLICANT: Krause, James
TITLE OF INVENTION: Chimer
FILE REFERENCE: N2000.001
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US-09-771-956-24
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SEQ ID NO 24
LENGTH: 499
TYPE: PRT
ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
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                                                                            CCLNPILYGFLNNGIK 338
                                                                                                      RIKKRSRSVFYRLTILILVFAVSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLLGMMS
                                                                                                                                                         LPAPAGPSQGKHLAVPENPASVRSQLSPSSKVIPGVPICFEVKPEESSDAHEMRVKRSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence:Y1/Y5 CHIMERA
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Pred. No. 1.3e-118;
0; Mismatches 18;
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CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 508
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-771-956-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.6%; Score 1461.5; DB 10; Length 508; Best Local Similarity 64.7%; Pred. No. 7.5e-117; Matches 295; Conservative 19; Mismatches 17; Indels 125; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
FILE REFERENCE: N2000.001
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                                                                              RHFKLVYCICHLLGMMSCCLNPILYGFLNNGIKADL 341
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    Issued_Patents_AA:*
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Copyright (c) 1993 - 2002 Compugen
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US-08-668-650B-14
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US-08-630-118A-6
US-09-235-839-6
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Query Match 90.9%; Score 1668.5; DB 1; Lengt Best Local Similarity 73.2%; Pred. No. 8.8e-135; Matches 333; Conservative 6; Mismatches 11; Indels	RESULT 1 US-08-349-025-4 US-08-349-025-4 Sequence 4, Application US/08349025 Patent No. 5602024 GENERAL INFORMATION: APPLICANT: Welker, Mary W. APPLICANT: Welker, Mary W. APPLICANT: Welshahak, Richard L. TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPIC, TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR NUMBER OF SEQUENCES: 4 CORRESSPONDENCE ADDRESS: ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of the Americas CITY: New York STATE: New York STATE: New York COMPUTER: LIBS Avenue of America COMPUTER: LIBS COMPAILIBLE FORM: MEDLUM TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDLUM TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDLUM TYPE: FLOPPY disk COMPUTER READABLE FORMS/MS-DOS SOFTWARE: PATENTION INFORMATION: APPLICATION NUMBER: US/08/349,025 FILING DATE: CURRENT APPLICATION DATA: APPLICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEPHONE: (212) 278-0400 TELEEX 42523 COOP UI INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 455 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein	ALIGNMENTS	28
h 455; 105;	OR (Y5) AND		Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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US-08-566-096A-4
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GENERAL INFORMATION:
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                                                                                 TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
   MOLECULE
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                               REFERENCE/DOCKET NUMBER: 17 TELECOMMUNICATION INFORMATION:
                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR,
TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALA
TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (YS) AND USES THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gerald, Christophe
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                               455 amino acids
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Walker, Mary W.
                                                                                                               (212) 278-0400
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US-08-668-650B-4
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Gerald, Christop
APPLICANT: Waker, Mary W.
APPLICANT: Wainshank, Riche
TITLE OF INVENTION: Method
TITLE OF INVENTION: Compou
TITLE OF INVENTION: Hypoth
TITLE OF INVENTION: Compou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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           NAME: White Esq., John P. REGISTRATION NUMBER: 28,6
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1185 Avenue
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                                                                            04-JUN-1996
NUMBER:
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Methods of Modifying Feeding Behavior,
Compounds Useful in Such Methods, And DNA Encoding
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of the
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Pred. No. 8.8
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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Weinshank, Richard L.
APPLICANT: Weinshank, Richard L.
APPLICANT: Walker, Mary W.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
TITILE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Use
TITLE OF INVENTION: Methods of Modifying Feeding A Hypothalamic
TITLE OF INVENTION: Methods, and DNA Encoding A Hypothalamic
TITLE OF INVENTION: Methods, and DNA Encoding A Hypothalamic
CURRENT APPLICATION NUMBER: US/09/200,673A
CURRENT FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: 08/566,096
EARLIER APPLICATION NUMBER: 08/349,025
EARLIER APPLICATION NUMBER: 08/349,025
EARLIER FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 17
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                                                     SOFTWARE: PatentIn
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09200673A Patent No. 6316203
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   ORGANISM: Homo
                                      LENGTH: 455
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TELEPHONE: 212-278-0400
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Pred. No. 8.8e-135;
5; Mismatches 11;
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RESULT 5
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                         REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                             TELEFAX:
                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: PatentI
                                           TELEPHONE:
                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                STREET: 1185 AVCCITY: New York
STATE: New York
                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       COUNTRY:
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                               (212)
                                                                                                                                                                                                                                                                                                                                                                                          Synaptic Pharmaceutical Corporation
VERWION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS
VERWION: USEBUL IN SUCH METHODS, AND DNA ENCODING A HYPOTH
VENTION: Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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RESULT 6
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TYPE: amino a
TOPOLOGY: lir
MOLECULE TYPE:
                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                           APPLICANT: Gerald, Christophe P.(APPLICANT: Waker, Mary W. APPLICANT: Branchek, Theresa APPLICANT: Weinshank, Richard L.
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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hes 333;
APPLICATION NUMBER: US/08/668,650B FILING DATE: 04-JUN-1996 CLASSIFICATION: 536
                                                                                                   MEDIUM TYPE:
                                                                                                                                               COUNTRY:
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Compounds Useful In Such Methods, And DNA Encoding a
Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor
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Pred. No. 8.8e-135;
                                                                                                                                                                                           Americas
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RESULT 7
US-08-630-118A-6
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                                                                                                                                                                                                                                                                                                Sequence 6,
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Best Local Similarity
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                             APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and
TITLE OF INVENTION: Sequences
                                                                                                                                                                                                                         APPLICANT: Hu Ph.D., x111
APPLICANT: McCaleb Ph.D.
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TOPOLOGY: linear
MOLECULE TYPE: protein
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REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166C
TELECOMMUNICATION INFORMATION:
                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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LENGTH: 456 amino acids
TYPE: amino acid
COMPUTER READABLE
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               ZIP:
                             COUNTRY:
                                                              ADDRESSEE: McDonners Louise, STREET: 300 South Wacker Drive,
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                                              STATE:
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)O South Wacker Drive, 32nd Floor
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 FORM:
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71.6%;
                                                                                                                                 Sequences
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h.D., Michael L.
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                                                                                                                                                                Nucleic
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                                                                                                                                                              Sequence 6, Application US/08838399 Patent No. 5965392
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Best Local Similarity
                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hu Ph.
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TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
TITLE OF INVENTION: Sequences
NUMBER OF SEQUENCES: 8
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NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: April 8, 1996
CLASSIFICATION: 435
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TOPOLOGY: linear
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                                                                                                                             Hu Ph.D.,
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72.6%;
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Pred. No. 4.2e-130;
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RESULT 9
US-09-003-199-21
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 445 amino acids
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NAME: Greenfield Ph.D., Michael S
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/W
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,39
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CITY: Chicago
STATE: IL
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CLASSIFICATION:
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Local Similarity 72.68;
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                                                                                                               NPILYGFLNNGIKADLVSLIHCLHM
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Pred. No. 4.2e
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GENERAL INFORMATION:

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Best Local Similarity 72.6%;
Matches 323; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
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MEDIUM TYPE: Diskette
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APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Thampoe, Immac J.
 421
                                                    266 SRSRSVEYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 325
                             326
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                                                                                                                                                                           241 GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                              11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Thampoe, Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CN0775
                                                                                                                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Kenilworth STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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               NPILYGFLNNGIKADLVSLIHCLHM 350
                                                                                                                 ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 360
                                                                                                                                                                                                      RLKRRNNMMDK - - - - - - - -
NPILYGFLNNGIKADLVSLIHCLHM 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1613.5; DB 2;
Pred. No. 4.2e-130;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 445;
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258MRDNKYR	Qy
241 GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP 300	Db
247 RLKRRNNMMD	Qy
191 VELQETYSSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCI 246	Db Qy
131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 19	Db Qy
71 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 130	Оy
/ 11 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 70 	Дy
Query Match 87.9%; Score 1613.5; DB 4; Length 445; Best Local Similarity 72.6%; Pred. No. 4.2e-130; Matches 323; Conservative 6; Mismatches 11; Indels 105; Gaps	
LENGTH: 445 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 5-09-235-839-6	US ;
MATIC 0001 02 : 6:	
NAME: Greenfield Ph.D., Michael S. REGISTRATION NUMBER: 37,142 REFERENCE/DOCKET NUMBER: 96,149-C	
8/630,118 1996 ON:	
APPLICATION NUMBER: US/09/235,839 FILING DATE: CLASSIFICATION:	
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	
COMPUTER: FLORDY disk MEDIUM TYPE: Florpy disk COMPUTER: IBM PC compatible	
STATE: IL COUNTRY: USA ZIP: 60606	
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago	
TITLE OF INVENTION: Neuropeptine i Receptor and Nucleic Acid NUMBER OF SEQUENCES: Sequences CORRESPONDENCE ADDRESS:	
D., Jaime R. Inda J.	
APPLICANT: Hu Ph.D., Yinghe APPLICANT: McCaleb Ph.D., Michael L. APPLICANT: Bloomquist Ph.D., Brian T.	
339-6 Apr	US.

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301 ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK

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US-09-327-035-6
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Best Local Similarity 72.6%;
Matches 323; Conservative
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                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 KRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 420
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                                                      APPLICANT: Hu Ph.D., Yinghe
McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.
Cornfield Ph.D., Linda J.
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/838,399
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/327,035
FILING DATE: 07-Un-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 300 SO
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
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pred. No. 4.2e-130;
6; Mismatches 11;
                                                                                                                                                                                                     Indels 105;
                                                                                                                                                                                                                                     Length 445;
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	MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 70 	11 1	Qy Db
ω	Ech 87.7%; Score 1610.5; DB 4; Length 445; al Similarity 72.4%; Pred. No. 7.5e-130; 322; Conservative 7; Mismatches 11; Indels 105; Gaps	Query Match Best Local Matches 32	
	MOLECULE TYPE: protein	MOLECI -09-040-	us
	lin	TOP	·. ·.
	ION FOR SEQ ID NO: 2:	INFORMA	
	TELEPHONE: (317) 276-0756 TELEPAX: (317) 276-1861	TEL	
	INFORMATIC	TELEC	
	NAME: Gaylo, Paul J. REGISTRATION NUMBER: 36,808	NAME:	
	Y/AGENT INFOR	ATTOR	
	70107	FIL	
	/040	CURRE	
	SOFTWARE: PatentIn Release #1.0, Version #1.30	SOF	
	BM PC compatible	COM	
	ER RE	COMPU	
	COUNTRY: United States of America ZIP: 46285	COUN ZIP:	·. ·.
	Indiana	STATE:	
	Lilly Corpora	STR	
	and	CORRE	
	NUMBER OF SEQUENCES: 5	NUMBE	•• ••
	Melvyn	APPLICANT:	•••
	GENERAL INFORMATION:	GENERAL	
	2, Application US/09040958	Sequence	
	58-2	SULT 12 -09-040-9	RE US
	PILYGFLNNGIKADLVSLIHCLHM 445	421	Db
	NPILYGELNNGIKADLVSLIHCLHM 350	326	Qy
	RSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 420	361	DЪ
	SRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 325	266	Qy
	ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 360	301	ДD
	MRDNKYR	258 -	Qy
	: ::: GLSNKENRLEENEMINLTLHPSKKSGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP 300	241	Db
		247	Qy
	VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240	181	дЬ
	ELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCI 246	191	Qy
	QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180	121	Db

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US-09-040-958-4
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                                                            Query Match
Best Local Similarity
Matches 322; Conserva
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Baez, 1
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-11350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y5 RECEPTOR NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                 TYPE: ami TOPOLOGY:
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266
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Lilly CorpoRITY: Indianapolis STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/040,958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 325
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Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                             Conservative
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                                                                                                                                                    linear
                                                                        87.78;
                                                         Score 1610.5; DB 4; Length 445;
Pred. No. 7.5e-130;
7; Mismatches 11; Indels 105;
                                                          Indels 105;
                                                          Gaps
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TELEPH TELEFA TELEFA ORMATIO
REGISTRATION NUMBER REFERENCE/DOCKET
CLASSIFICATION: ATTORNEY/AGENT INFO
OPERATING SYSTEM: Macint SOFTWARE: Microsoft Word
COUNTRY: USA ZIP: 07033-053
STATE: NJ
ADDRESSEE: Scherin STREET: 2000 Gallo
NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
APPLICANT: Rudinski, Mark S TITLE OF INVENTION: CHIMERIC M
APPLICANT: Parker, APPLICANT: Strader,
Patent No. 5985616 GENERAL INFORMATION:
to H
Db 421 NPILYGELNNGIKADLMSLIHCLHM 445
Qy 326 NPILYGFLNNGIKADLVSLIHCLHM 350
Db 361 KRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 420
Qy 266 SRSRSVFYRLTILILLVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCL 325
Db 301 ERPSQENHSRILPENFGSVRSQLSSSSKFIPGVPTCFEIKPEENSDVHELRVKRSVTRIK 360
QY 258MRDNKYRS 265
: ::: Db 241 GLSNKENRLEENEMINLTLHPSRKIGPQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPAP 300
QY 247 RLKRRNNMMDK 257
191 VELQETEGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCI
Qy 131 QCVSVLVSTLLLISIALVRYHNIKHPISNULTANHQYELLARVWTLGEAICSPLPVEHSL 190
ol LilmalmakkuQXTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLUQWMFGKVMCHLMPFL 1
71 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQMMFGKVMCHIMPFL 13

Best Local Similarity 69.2 Matches 308; Conservative

69.2%;

Pred. No. 1.2e-124; 4; Mismatches 18;

Indels

105;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                     REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES
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                                                         TELEFAX:
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US-08-349-025-2
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Best Local
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                                                                                            LPAPAGPSQGKHLAVPENPASVRSQLSPSSKVIPGVPICFEVKPEESSDAHEMRVKRSIT
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67.9%; Pred. No. 1.8e-123;
tive 21; Mismatches 19;
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